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Study of correlation in pearl millet

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Abstract
The study was conducted to determine the correlation in 60 seed parents (maintainer lines) and hybrids of pearl millet which were evaluated during *kharif* (Rainy) season 2021. Since selection for one character results in unintended changes in other characters, correlation studies are used to determine whether selected features are suitable for indirect selection. Yield is a complex quantitative variable that is strongly influenced by the environment, so direct selection for yield is ineffective. The relationship between yield and its component qualities, as well as among themselves, is therefore crucial in selection programs. Vigour index –I was highly positively correlated with G%, RL, SL, Seed L, Dry weight, V-II and PH while highly negatively correlated with PL, PD. Vigour index –II was found highly positively correlated with seedling length, shoot length, vigour index –I, dry weight, G%, root length, 1000 SW and PH.

Keywords: Correlation, maintainer lines, pearl millet, seed vigour, grain yield

Introduction
Pearl millet [*Pennisetum glaucum* (L.) R. Br.], is an annual diploid (2n=2x=14) plant of the family *Poaceae* and is commonly known as Bajra, Cumbu, Cat tail millet and Bulrush millet in different fragments of the world. It is a C_4 monocot species and highly cross pollinated. It is a resilient and dependable energy source and an excellent source of other dietary needs, especially micronutrients. Since selection for one character results in unintended changes in other characters, correlation studies are used to determine whether selected features are suitable for indirect selection. Because yield is a complex quantitative variable that is strongly influenced by the environment, direct selection for yield is ineffective. The relationship between yield and its component qualities, as well as among themselves, is therefore crucial in selection programs.

Material and Methods
The research study was carried out with a total of 60 seed parents (maintainer lines) and hybrids of pearl millet which were evaluated during *kharif* (Rainy) season 2021. The genotypes were evaluated in Randomized Block Design (RBD) with two replications. Each genotype was planted in single row plot of 4 meter length with row to row spacing of 45cm during *kharif* (Rainy) 2020. Plant to plant distance was 10 cm to 12 cm. All the recommended package of practices were followed to raise good crop. The analysis was carried out for eight agro morphological traits and two biochemical traits, and five seed parameters. Phenotypic and genotypic coefficients of correlation between two traits were estimated as per the formula proposed by Al-Jibouri *et al.* (1958) [1].

Results and Discussion
The phenotypic correlation coefficients of grain yield and other component traits, as well as between themselves, are displayed in Table 1 while Fig I describes the estimates of phenotypic correlations for days to 50% flowering (DF), plant height (PH), panicle diameter (PD) and panicle length (PD) with other agro-morphological, seed and biochemical characters in pearl millet germplasm lines, Fig II for number of productive tillers/ plant (NPT) 1000 Seed Weight (1000 SW), Dry fodder yield/ plant (DRY F) and Comprehensive Acid Value 0 (CAV 0) with other agro-morphological, seed and biochemical characters in pearl millet germplasm lines, Fig III for Comprehensive Acid Value (CAV 10), CAV diff, Comprehensive Peroxide Value 0 (CPV 0) and Comprehensive Peroxide Value 10 (CPV 10) with other agro-morphological, seed and biochemical characters in pearl millet germplasm lines, Fig IV for CPV diff, germination percentage (G%), Root length (RL) and Shoot length (SL) with other

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agro-morphological, seed and biochemical characters in pearl millet germplasm lines and lastly Fig V for seedling length (SEED L), DRY WT, Vigour index –I (V-I), Vigour index-II (V-II) and Grain yield/ plant (GY) with other agro-morphological, seed and biochemical characters in pearl millet germplasm lines.

Singh *et al.* (2018) [9] assessed 34 pearl millet germplasm lines for the association between grain yield and component traits. Indirect selection can be used in breeding programs to increase grain output for the traits number of effective tillers per plant, ear length, ear girth, and seed density as they showed a positive correlation with grain yield. The findings of Kumar *et al.* (2014) [7], Ezeaku *et al.* (2014) [5] and Pallavi *et al.* (2020) [8] revealed the positive association of plant height with grain yield/plant which were also found in present investigation. Bhasker *et al.* (2018) [3], Anuradha *et al.* (2018) [2] and Kaushik *et al.* (2018) [6] also reported significant positive correlation of 1000 seed weight with grain yield/plant.

There is a strong intrinsic relationship between various attributes, as evidenced by the magnitudes of correlation coefficients for almost all qualities at the genotypic level being greater than their phenotypic level counterparts. Correlation coefficients were calculated to study the association among different characters and are presented in table 1.

1.1 Days to 50% flowering
Days to 50% flowering expressed significant positive correlation with the panicle diameter $r_p=0.293$) at phenotypic levels. (Table 1).

1.2 Plant height
Plant height expressed significant positive correlation with the panicle length ($r_g=0.322$), G % ($r_p=0.307$), SL ($r_p=0.217$), Dry wt ($r_p=0.345$), V-I ($r_p=0.263$), V-II ($r_p=0.401$), GY ($r_p=0.294$) at phenotypic levels (Table 1).

1.3 Panicle Length
Panicle length expressed significant positive correlation for DF ($r_p=0.293$), 1000 SW ($r_p=0.289$) at phenotypic levels. However, with SL ($r_p=-0.199$), Seed L ($r_p=-0.346$), V-I ($r_p=-0.329$) it was negatively and significantly correlated at phenotypic levels (Table 1).

1.4 1000 Seed Weight
1000 seed weight expressed significant positive correlation with PD ($r_p=0.289$), Dry wt ($r_p=0.367$), V-II ($r_p=0.309$) at phenotypic levels. However, with CAV 0 ($r_p=-0.198$), it was negatively and significantly correlated at phenotypic levels (Table 1).

1.5 Dry Fodder Yield/Plant
Dry fodder yield/plant expressed significant positive correlation with CPV diff ($r_p=0.265$), SL ($r_p=0.196$), Seed L ($r_p=0.232$) at phenotypic levels (Table 1).

1.6 CAV 0
CAV 0 expressed significant positive correlation with CPV 0 ($r_p=0.252$), CPV 10 ($r_p=0.214$) at phenotypic levels. However, with 1000 SW ($r_p=-0.198$), GY ($r_p=-0.373$) it was negatively and significantly correlated at phenotypic levels (Table 1).

1.7 CAV 10
CAV 10 expressed significant positive correlation with CAV diff ($r_p=0.523$), CPV 10 ($r_p=0.225$), CPV diff ($r_p=0.294$) at phenotypic levels. However, with CPV 0 ($r_p=-0.222$), GY ($r_p=-0.196$) it was negatively and significantly correlated at phenotypic levels (Table 1).

1.8 CAV difference
CAV difference expressed significant positive correlation with PL ($r_p=0.192$), CAV 10 ($r_p=0.523$), CPV 10 ($r_p=0.261$) at phenotypic levels. However, with CPV 0($r_p=-0.230$), GY ($r_p=-0.19$) it was negatively and significantly correlated at phenotypic levels (Table 1).

1.9 CPV 0
CPV 0 expressed significant positive correlation with CAV 0 ($r_p=0.252$) at phenotypic levels. However, with CAV 10 ($r_p=-0.222$), CAV diff ($r_p=-0.230$), GY ($r_p=-0.203$), CPV diff ($r_p=-0.189$) it was negatively and significantly correlated at phenotypic levels (Table 1).

1.10 CPV 10
CPV 10 expressed significant positive correlation with CAV 0 ($r_p=0.214$), CAV 10 ($r_p=0.225$), CAV diff ($r_p=0.261$), CPV diff ($r_p=0.333$) at phenotypic levels. (Table 1).

1.11 CPV difference
CPV difference expressed significant positive correlation with Dry F ($r_p=0.265$), CAV 10 ($r_p=0.294$), CPV 10 ($r_p=0.333$) at phenotypic levels. However, with CPV 0 ($r_p=-0.189$) it was negatively and significantly correlated at phenotypic levels (Table 1).

1.12 Germination %
Germination % expressed significant positive correlation with PH ($r_p=0.307$), RL ($r_p=0.359$), SL ($r_p=494$), Seed L ($r_p=0.511$), Dry wt ($r_p=0.436$), V-I ($r_p=0.91$), V-II ($r_p=0.763$), GY ($r_p=0.201$) at phenotypic levels. However, with PL ($r_p=-0.224$), it was negatively and significantly correlated at phenotypic levels (Table 1).

1.13 Root length
Root length expressed significant positive correlation with Dry F ($r_p=0.189$), G% ($r_p=0.359$), SL ($r_p=0.381$), SEED L ($r_p=0.842$), V-I ($r_p=0.643$), V-II ($r_p=0.291$) at phenotypic levels. However, with PL ($r_p=-0.359$), it was negatively and significantly correlated at phenotypic levels (Table 1).

1.14 Shoot length
Shoot length expressed significant positive correlation with PH ($r_p=0.217$), Dry F ($r_p=0.196$), G% ($r_p=0.494$), RL ($r_p=0.381$), SEED L ($r_p=0.819$), DRY WT ($r_p=0.341$), V-I ($r_p=0.704$), V-II ($r_p=0.466$), GY ($r_p=0.265$) at phenotypic levels. However, with PD ($r_p=-0.199$), PL ($r_p=-0.212$), it was negatively and significantly correlated at phenotypic levels (Table 1).

1.15 Seedling length
Seedling length expressed significant positive correlation with Dry F ($r_p=0.232$), G% ($r_p=0.511$), RL ($r_p=0.842$), SL ($r_p=0.819$), Dry wt ($r_p=0.310$), V-I ($r_p=0.809$), V-II ($r_p=0.452$), GY ($r_p=0.180$) at phenotypic levels. However, PD ($r_p=-0.218$), PL ($r_p=-0.346$) was negatively and significantly correlated at phenotypic levels (Table 1).

1.16 Dry weight

Dry weight expressed significant positive correlation with PH (r_p=0.345), 1000 SW (r_p=0.367), G% (r_p=0.436), SL (r_p=0.341), SEED L (r_p=0.310), V-I (r_p=0.444), V-II (r_p=0.894), GY (r_p=0.242) at phenotypic levels (Table 1).

1.17 Vigour index I

Vigour index I expressed significant positive correlation with PH (r_p=0.263), G% (r_p=0.91), RL (r_p=0.643), SL (r_p=0.704), SEED L (r_p=0.809), Dry Wt (r_p=0.444), V-II (r_p=0.734), GY (r_p=0.222) at phenotypic levels. However, with PD (r_p= -0.207), PL (r_p= -0.329) it was negatively and significantly correlated at phenotypic levels (Table 1).

1.18 Vigour index II

Vigour index II expressed significant positive correlation with PH (r_p=0.401), 1000 SW (r_p=0.309), G% (r_p=0.763), RL (r_p=0.291), SL (r_p=0.466), SEED L (r_p=0.452), Dry wt. (r_p=0.894), V-I (r_p=0.734), GY (r_p=0.304) at phenotypic levels (Table 1).

1.19 Grain yield / plant

Grain yield / plant expressed significant positive correlation with 1000 SW (r_p=0.278), PH (r_p= 0.294), G% (r_p=0.201), SL (r_p= 0.265), SEED L (r_p=0.180), DRY WT (r_p=0.242), V-I (r_p=0.222), V-II (r_p=0.304) at phenotypic levels. However, with CAV 0 (r_p= -0.373), CAV diff (r_p= -0.190), CAV 10 (r_p= -0.196), CPV 0 (r_p= -0.203) it was negatively and significantly correlated at phenotypic levels (Table 1).

Table 1: Estimates for phenotypic correlation coefficients for agro morphological, seed and biochemical traits in pearl millet germplasm lines

TRAITS	DF	PH	PD	PL	NPT	1000 SW	DRY F	CAV 0	CAV10	CAV diff	CPV 0	CPV10
DF	1											
PH	-0.074	1										
PD	0.293**	-0.026	1									
PL	0.154	0.157	0.173	1								
NPT	0.094	0.04	-0.127	0.057	1							
1000 SW	-0.038	0.158	0.289**	-0.11	0.149	1						
DRY F	0.153	0.086	0.022	-0.129	-0.06	-0.16	1					
CAV 0	0.13	-0.076	0.023	0.02	0.009	-0.198*	-0.134	1				
CAV10	0.053	-0.161	-0.07	0.039	0.032	0.067	-0.057	-0.022	1			
cav diff	0.1	-0.125	0.037	0.192*	-0.018	-0.075	-0.099	0.097	0.523**	1		
CPV 0	-0.016	-0.029	0.164	-0.166	-0.053	0.061	-0.075	0.252**	-0.222*	-0.230*	1	
CPV10	-0.102	0.057	0.044	0.166	0.011	0.099	-0.068	0.214*	0.225*	0.261**	0.136	1
cpv diff	0.019	0.068	-0.065	0.119	0.083	-0.027	0.265**	-0.098	0.294**	0.109	-0.189*	0.333**
G%	0.038	0.307**	-0.172	-0.224*	0.117	0.112	-0.033	0.075	-0.004	-0.087	-0.015	-0.143
RL	-0.138	0.006	-0.165	-0.359**	0.074	0.069	0.189*	0.121	-0.042	-0.095	0.064	-0.101
SL	-0.107	0.217*	-0.199*	-0.212*	0.177	0.056	0.196*	-0.167	-0.126	-0.17	0.037	-0.085
SEED L	-0.148	0.131	-0.218*	-0.346**	0.149	0.076	0.232*	-0.022	-0.1	-0.158	0.061	-0.112
DRY WT	-0.132	0.345**	0.081	0.06	0.065	0.367**	-0.043	0.024	-0.001	-0.077	0.01	0.051
V-I	-0.053	0.263**	-0.207*	-0.329**	0.145	0.137	0.076	0.046	-0.053	-0.149	0.022	-0.168
V-II	-0.09	0.401**	-0.023	-0.08	0.066	0.309**	-0.067	0.048	-0.019	-0.1	-0.001	-0.057
GY	0.03	0.294**	0.036	-0.119	0.123	0.278**	0.031	-0.373**	-0.196*	-0.190*	-0.203*	-0.101

TRAITS	cpv diff	G%	RL	SL	SEED L	DRY WT	V-I	V-II	GY
DF									
PH									
PD									
PL									
NPT									
1000 SW									
DRY F									
CAV 0									
CAV10									
cav diff									
CPV 0									
CPV10									
cpv diff	1								
G%	-0.066	1							
RL	0.093	0.359**	1						
SL	0.161	0.494**	0.381**	1					
SEED L	0.151	0.511**	0.842**	0.819**	1				
DRY WT	0.055	0.436**	0.179	0.341**	0.310**	1			
V-I	-0.005	0.910**	0.643**	0.704**	0.809**	0.444**	1		
V-II	-0.028	0.763**	0.291**	0.466**	0.452**	0.894**	0.734**	1	
GY	-0.007	0.201*	0.041	0.265**	0.180*	0.242**	0.222*	0.304**	1

r_p are phenotypic coefficient, respectively, * Significant at p = 0.05, ** Significant at p = 0.01

CAV 0- Comprehensive Acid Value on the first day, CAV 10- Comprehensive Acid Value on the 10th day, CAV diff-

Difference between CAV on 1st and 10th day, CPV 0- Comprehensive Peroxide Value on the first day, CPV 10-

Comprehensive Peroxide Value on the 10th day, CPV diff-Difference between CPV on 1st and 10th day, DRY WT-Seedling dry weight (mg), Dry F- Dry fodder yield/ plant (g), PL- Panicle length (cm), PD- Panicle diameter (cm), NPT-No. of productive tillers /plant, PH- Plant height (cm), GY-Grain yield /plant (g), RL- Root length (cm), SL- Shoot length(cm), SEED L- Seedling length(cm), V-I- Vigour index I, V-II- Vigour index II, 1000 SW- 1000 seed weight (g), G%-Germination percent(%), DF-Days to 50% flowering
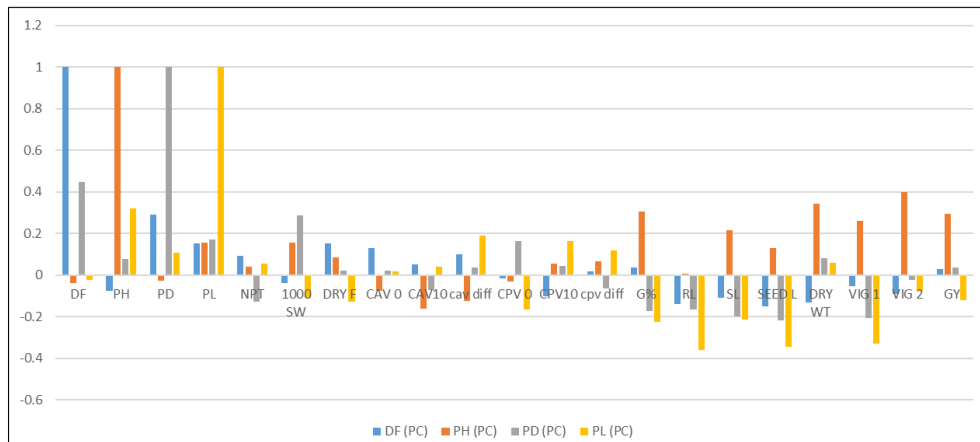

Fig 1: Estimates of genotypic and phenotypic correlations for days to 50% flowering (DF), plant height (PH), panicle diameter (PD) and panicle length (PD) with other agro-morphological, seed and biochemical characters in pearl millet germplasm lines
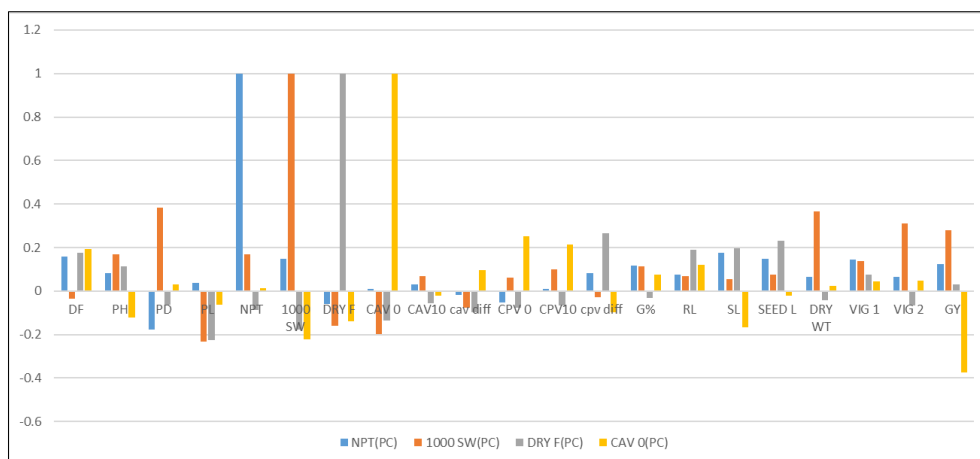

Fig 2: Estimates of genotypic and phenotypic correlations for number of productive tillers/ plant(NPT) 1000 Seed Weight(1000 SW), Dry fodder yield/ plant(DRY F) and Comprehensive Acid Value 0(CAV 0) with other agro-morphological, seed and biochemical characters in pearl millet germplasm lines
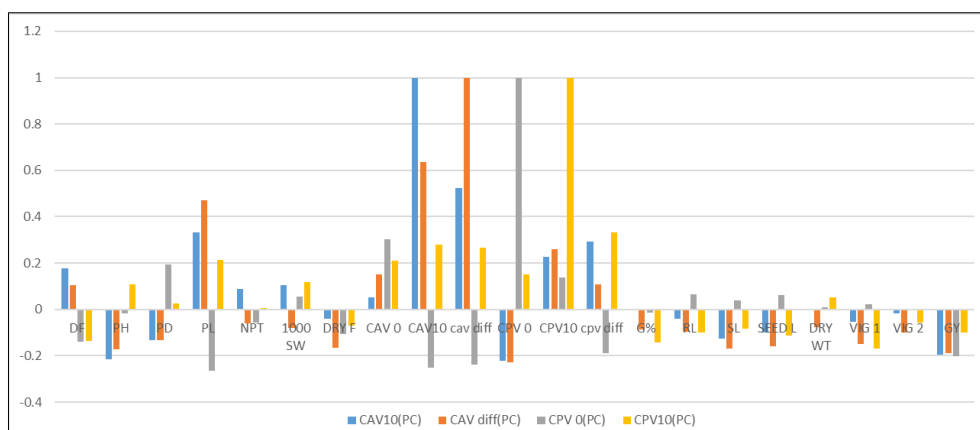

Fig 3: Estimates of genotypic and phenotypic correlations for Comprehensive Acid Value (CAV 10), CAV diff, Comprehensive Peroxide Value 0 (CPV 0) and Comprehensive Peroxide Value 10 (CPV 10) with other agro-morphological, seed and biochemical characters in pearl millet germplasm lines
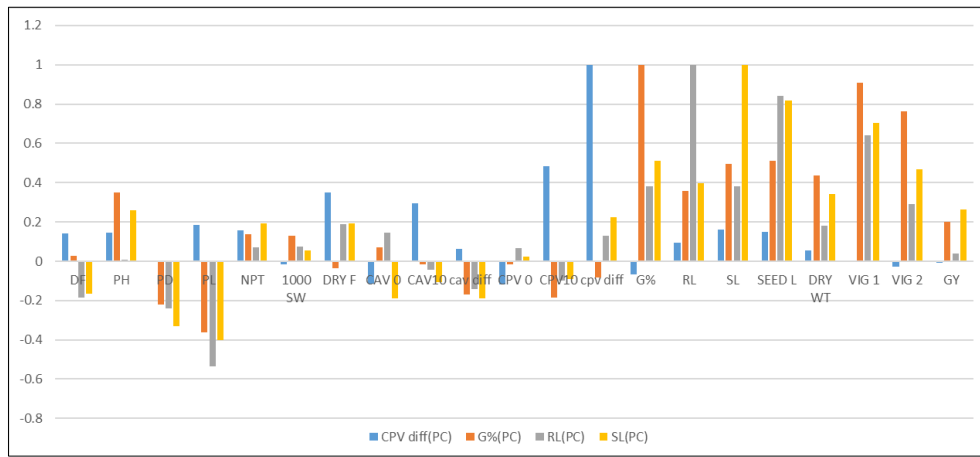
Fig 4: Estimates of genotypic and phenotypic correlations for CPV diff, germination percentage(G%), Root length(RL) and Shoot length(SL) with other agro-morphological, seed and biochemical characters in pearl millet germplasm lines
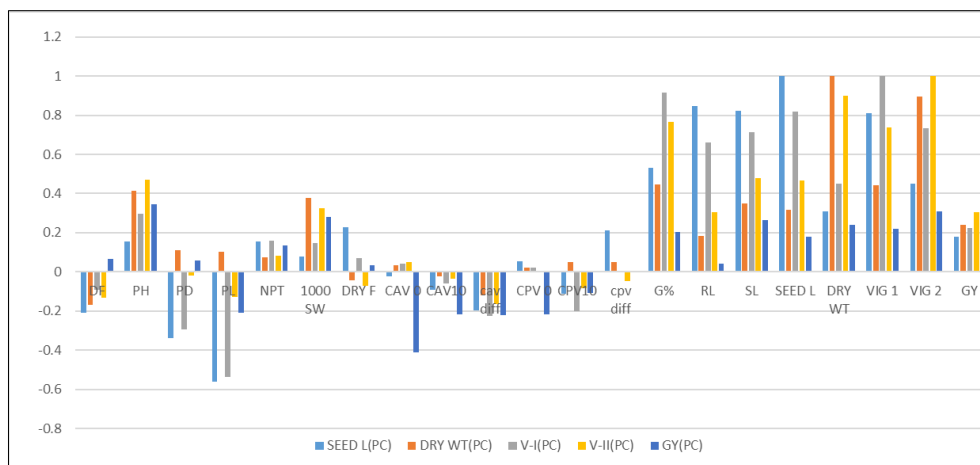

Fig 5: Estimates of genotypic and phenotypic correlations for seedling length (SEED L), DRY WT, Vigour index –I (V-I), Vigour index- II (V-II) and Grain yield/ plant (GY) with other agro-morphological, seed and biochemical characters in pearl millet germplasm lines

Conclusion
The magnitudes of correlation coefficients for almost all attributes at the genotypic level were greater than their corresponding phenotypic level, indicating strong inherent relation of these traits with grain yield. The traits *viz*., No of Productive Tillers/plant, 1000 Seed Weight, Dry Fodder yield/plant, CAV 0, CAV 10, CPV 0, CPV 10, Germination %, Shoot Length, Germination % (0.204), seedling dry weight (0.242), V-I (0.221), V-II (0.307) and Plant Height (0.346) exhibited positive and significant association with grain yield/plant indicating selection of these traits would be desirable pearl millet improvement programs.

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